

sequencelisting-21407.ST25
SEQUENCE LISTING

<110> Roche Vitamins AG

<120> SQS gene

<130> NDR5218

<160> 8

<170> PatentIn version 3.1

<210> 1

<211> 4807

<212> DNA

<213> Phaffia rhodozyma

<220>

<221> exon

<222> (1550)..(1577)

<223>

<220>

<221> polyA_site

<222> (4106)..(4107)

<223>

<220>

<221> 5'UTR

<222> (1469)..(1470)

<223>

<220>

<221> exon

sequencelisting-21407.ST25

<222> (3959)..(3970)

<223>

<220>

<221> Intron

<222> (3882)..(3958)

<223>

<220>

<221> exon

<222> (3567)..(3881)

<223>

<220>

<221> Intron

<222> (3476)..(3564)

<223>

<220>

<221> exon

<222> (3454)..(3474)

<223>

<220>

<221> Intron

<222> (3357)..(3453)

<223>

<220>

<221> exon

<222> (3231)..(3356)

<223>

<220>

sequencelisting-21407.ST25

<221> Intron
<222> (3088)..(3230)
<223>

<220>
<221> exon
<222> (2476)..(3087)
<223>

<220>
<221> Intron
<222> (2398)..(2474)
<223>

<220>
<221> exon
<222> (2183)..(2395)
<223>

<220>
<221> Intron
<222> (2072)..(2182)
<223>

<220>
<221> exon
<222> (1883)..(2071)
<223>

<220>
<221> Intron
<222> (1767)..(1882)
<223>

sequence listing-21407.ST25

<220>

<221> exon

<222> (1755)..(1766)

<223>

<220>

<221> Intron

<222> (1578)..(1752)

<223>

<400> 1

gttcctgttc agtcaaagag tgggaaaaac atgaaagtaa aaagatgtaa tgaaagaagg	60
ggtcagaaca tcggagatac aatggcccat agaggaagga aagctactta ccagaaacca	120
gtgaggtttg cctaggaagt aatcccttcg tttctcaaag atatcttttt tgaaagcatc	180
gatgaacgac atgtcgaacc catctccatc ctcgaaatca agtttactcg atttagacct	240
ttccagcttt tctgctctct ccagtttcgc agctttctct tcgggaagaa gctctccgcc	300
agtcgatgtt ctgtcgacag gagaccagta gaaggcggaa ccgacaattt tggatggatc	360
ggaggacagg gtggctttaa caaatcggta gtacggagga tcgaacggcg cttctctcgt	420
tcgaaggttg actcctcttg ctatgtgtat gagagcatat ccgttgatgt ctcagttaaa	480
atttcctttt ctttctaccc ggagagtaag acacacaaag aatcacgaag aatatgatga	540
ctgaccgatc cgaatatcta gcgcaggttg cttctctact ggttccattc ttcgaacgat	600
aggttcatgt ttgaaagcat tgatcctagt tgcctctatc tgaggccagt ctgccaatgt	660
agcaggctca atgatcactt ggggtttgtg catcttgatg ttcaaccaag tgtcgcaacg	720
gtcgagattc ttttttcttc ttttggtcga gaaaaaaaaa cggcttcgct tcgcacgcgc	780
gcgggggatc acccgcatat taagcggat gacgctcatc aaccggccaa gtgttcttca	840
tcataggtga aggttaaaac ggaatggata ggaggagcta accacgtttt tattttaatt	900
cgacttgggc agcctcgtcc atagtgtctg atggttatat cgtcatagaa aggcagcgcc	960
tggcgggttc gtcatggccg tgatcatctg ctttgttaga cattgtccat cagtcacctc	1020
aatgacagtt tcccgcgcc atcactaaga cacaaacgta tccagcacgc catgtccatc	1080
actgaagaag gtagggcttc gtcgagccag tgcaaccaga gttacagatg aacatcaggc	1140
cttgatcaga cccgacttat gaatatggcc gttattgtac acttcttggg gtcctcagag	1200
ctgctctttc gtgtttttca ctttctttcc ggatcaaacg agactgctcg tgtatctatc	1260
tgtgcttgcc atatgagcat cccatgcctc tgctcaaatg atgctggagc tacgatccat	1320
cagagacgac acaaaacggg gttgtatgaa ctctacattt cctaattgta ttggaatttt	1380
ctgtaatgcg ttcttcatct ttctctaattg cttttttgta gtccgtcttt tcaaccttgc	1440

cagcgtttcg	cgtgtcttct	ttctcctttg	acgggtcatca	ctttcttctc	tcttctcgtt	1500
ctttcttccg	tccttccttc	tctctcttcg	tctgaacatc	agcatcatc	atg ggc ata Met Gly Ile 1	1558
tca gat tac ctc gtt ctg g	gtcagttctg	tcttttgttt	gattcttctc			1607
Ser Asp Tyr Leu Val Leu						
5						
ttcttgccgg	cggtcgcctg	tcttggggtat	atcatcagca	atgagaaaca	tgatgttccc	1667
cccgcgtcaa	tcactgacct	tttggtcctc	tacttctttc	ctgtcgaatt	gatcctgatt	1727
gatacgtgtg	ccggctgctt	aacagct tt	cac gca tcc t	gtaggtgttt		1776
		Val His Ala Ser				
tatcgtatgc	ttcatgttga	tgtttagtca	cgcggactga	cctggccggt	tgattttctg	1836
tatgatcgct	tgtgctaccg	tctttcttgg	aaatccttcc	catcag gc	cga tct Cys Arg Ser 15	1890
gcg agc ttt aat gca gta cgc gat ctg gca tga gcc tcg aag gaa tat						1938
Ala Ser Phe Asn Ala Val Arg Asp Leu Ala					Ala Ser Lys Glu Tyr 30	
20						
25						
cac tgc aca gga gga aca tgc aac atc cgg ttg gga ccg aga aac tat						1986
His Cys Thr Gly Gly Thr Cys Asn Ile Arg Leu Gly Pro Arg Asn Tyr						
35						
40						
45						
gaa gga atg ttg gaa gta ttt gga tct gac ttc aag aag ttt cgc agc						2034
Glu Gly Met Leu Glu Val Phe Gly Ser Asp Phe Lys Lys Phe Arg Ser						
50						
55						
60						
tgt cat caa aga gtt gga cgg aga tct tac ccg agt c gtacgtgttt						2081
Cys His Gln Arg Val Gly Arg Arg Ser Tyr Pro Ser						
65						
70						
75						
tcaccttctc	tctcctttga	gatctggtcg	cctccgcatt	ttcttggtgc	agaagggtca	2141
gaagctgaca	acaccatctc	tactgttcgg	gacacggcta	g at	ctg ttt att cta His Leu Phe Ile Leu 80	2196
tct cgc tct tcg agg act gga tac cat tga gga tga cat gag tct atc						2244
Ser Arg Ser Ser Arg Thr Gly Tyr His					His Glu Ser Ile	
85						
90						
taa tga tgt gaa gct tcc cct gct tcg gac att ctg gga aaa gct tga						2292
Cys Glu Ala Ser Pro Ala Ser Asp Ile Leu Gly Lys Ala						
95						
100						
105						
ctc ccc tgg gtg gac ctt tac tgg atc cgg tcc aaa tga gaa gga tag						2340
Leu Pro Trp Val Asp Leu Tyr Trp Ile Arg Ser Lys					Glu Gly	
110						
115						
120						
aga gct tct tgt tca ctt cga tgt ggc cat cgc cga gtt tgc caa ctt						2388
Arg Ala Ser Cys Ser Leu Arg Cys Gly His Arg Arg Val Cys Gln Leu						
125						
130						
135						
gga cgt c aagtgagttt ccctttatgg ttggatcatc cgctcgacag actcgaaacg						2445
Gly Arg						
ctcatcactt	tggtctgctt	gatgaacagc	tc	tcg gaa cgt cat tcg aga cat		2498

sequencelisting-21407.ST25

Leu Ser Glu Arg His Ser Arg His
145

cac tcg caa gat ggg taa cgg tat ggc cga ctt tgc ttc tct ctc tac	2546
His Ser Gln Asp Gly Arg Tyr Gly Arg Leu Cys Phe Ser Leu Tyr	
150 155 160	
gcc ctc caa gcc tgt ggc cga ggt cca gtc gac cga aga ttt caa cct	2594
Ala Leu Gln Ala Cys Gly Arg Gly Pro Val Asp Arg Arg Phe Gln Pro	
165 170 175	
ata ctg tca tta cgt cgc tgg act cgt cgg cga ggg act ctc ccg act	2642
Ile Leu Ser Leu Arg Arg Trp Thr Arg Arg Arg Gly Thr Leu Pro Thr	
180 185 190	
ctt tgt cgc gac cga gaa gga acg acc att ctt ggc caa cca gat ggt	2690
Leu Cys Arg Asp Arg Glu Gly Thr Thr Ile Leu Gly Gln Pro Asp Gly	
195 200 205 210	
act ttc aaa ctc gtt cgg act cct tct cca aaa gac aaa cat cct tcg	2738
Thr Phe Lys Leu Val Arg Thr Pro Ser Pro Lys Asp Lys His Pro Ser	
215 220 225	
aga tat tcg gga gga cgc cga cga agg tcg tgg ctt ctg gcc aag aga	2786
Arg Tyr Ser Gly Gly Arg Arg Arg Arg Ser Trp Leu Leu Ala Lys Arg	
230 235 240	
gat ctg ggc caa ccc gat cta tac tgc gca tgc acc ggg cac aag gtt	2834
Asp Leu Gly Gln Pro Asp Leu Tyr Cys Ala Cys Thr Gly His Lys Val	
245 250 255	
taa ctc gtt gac tga cct ggt caa gaa aga aaa cat cga caa agg atc	2882
Leu Val Asp Pro Gly Gln Glu Arg Lys His Arg Gln Arg Ile	
260 265 270	
aat gtg ggt gtt gag tgc gat gac act cga cgc gat cac cca tac tac	2930
Asn Val Gly Val Glu Cys Asp Asp Thr Arg Arg Asp His Pro Tyr Tyr	
275 280 285	
cga cgc act gga cta cct ctc act tct aaa gaa cca gag tgt ttt caa	2978
Arg Arg Thr Gly Leu Pro Leu Thr Ser Lys Glu Pro Glu Cys Phe Gln	
290 295 300	
ctt ttg tgc tat ccc ggc tgt cat gtc gat tgc aac gtt gga gct atg	3026
Leu Leu Cys Tyr Pro Gly Cys His Val Asp Cys Asn Val Gly Ala Met	
305 310 315 320	
ctt cat gaa ccc agc ggt gtt cca acg aaa cat aaa aat cag aaa ggg	3074
Leu His Glu Pro Ser Gly Val Pro Thr Lys His Lys Asn Gln Lys Gly	
325 330 335	
aga agc cgt cga g gtgcgttcgc gcgttctgtt tctacctttc ataacattgg	3127
Arg Ser Arg Arg	
340	
aggttcttga ctcttaagcg tcttccaatc tgatgcctcc aattatcatc atttttgtct	3187
tttttgcttt cctcttgttt cttttcggcg tgattcaatc cag ct cat tat gaa	3241
Ala His Tyr Glu	
gtg caa caa ccc tcg gga ggt ggc ata cat gtt tag aga tta tgc tcg	3289
Val Gln Gln Pro Ser Gly Gly Gly Ile His Val Arg Leu Cys Ser	
345 350 355	
aaa gat tca tgc caa ggc tat tcc tac aga tcc taa ctt cat caa gtt	3337
Lys Asp Ser Cys Gln Gly Tyr Ser Tyr Arg Ser Leu His Gln Val	
360 365 370	

sequencelisting-21407.ST25

gag cgt tgc gtg tgg tcg a gtgagttgat cgatcgatcc atcttttgtt 3386
 Glu Arg Cys Val Trp Ser
 375 380

ttgatcatcg cgagacttga ctgatcgatt actcaaaaca tcatcgcttc tccttcttgc 3446
 tctctag at cga aca atg ggc tga gca c tgtatgttcc tccgcccctc 3494
 Asn Arg Thr Met Gly Ala
 385

cttcaagttt cctctcgctt catctttgtt gagaagaggg atctgatgta tctttctttg 3554
 ttcggatcag ac ta ccc ctc att tat gat gat tcg gcc ttc gaa tga ccc 3604
 Leu Pro Leu Ile Tyr Asp Asp Ser Ala Phe Glu Pro
 390 395

tca aaa ccc cgc acc ctc aac ggc gct tga ccc ttt ctc agg aga cgc 3652
 Ser Lys Pro Arg Thr Leu Asn Gly Ala Pro Phe Leu Arg Arg Arg
 400 405 410

tcg ttt aag gat agc ctc taa gaa ggc tga gat cac cgc cgc tgc tct 3700
 Ser Phe Lys Asp Ser Leu Glu Gly Asp His Arg Arg Cys Ser
 415 420 425

tgt cag gaa gaa agc ccg gga tca cgc taa gtg gag aga gtc caa ggg 3748
 Cys Gln Glu Glu Ser Pro Gly Ser Arg Val Glu Arg Val Gln Gly
 430 435 440

att gcc tcc gag cga tcc gaa caa gcc gga caa ctc gga gga tgt taa 3796
 Ile Ala Ser Glu Arg Ser Glu Gln Ala Gly Gln Leu Gly Gly Cys
 445 450 455

ttg ggt att gat cgg cgg tat gat cgt tgg att gtt gct cgt gat ggg 3844
 Leu Gly Ile Asp Arg Arg Tyr Asp Arg Trp Ile Val Ala Arg Asp Gly
 460 465 470

cgt gct cgg ttt ggc tat cgc ttg ggt tgt tct tca g gtgcgttctt 3891
 Arg Ala Arg Phe Gly Tyr Arg Leu Gly Cys Ser Ser
 475 480 485

ccaaagagcc tttctctcat gaacacgcac atagggttgat ctaattctat cttactctgt 3951
 catacag tt tga gca ata a tctcaagatt ctagtccatc ctttcgctca 4000
 Val Ala Ile

acgatctgct tcttctcctt ctccttctcc gtcttctctg gtttcttttc ttactttctg 4060
 ggatcttcct tcttgaatcc tccgatccaa tgtaatctgc ataccctcgc tttagtagaa 4120
 accgatcctt cattcgatct tggcgaaaat ctaagcaaag agaatcactt ttgtctaata 4180
 aaatttcctt taaagagtcg gctttttctt gtggcgaagc ttcaccccgt cttcctctgg 4240
 accatctctt ctcaatattc tttgtgctac tatatgatca agttctttga aatcaaagaa 4300
 gaacatgtat ttgattttga ggttccaaga atacaaccgg cccaagtcgt tcttcgcagt 4360
 tttcatcaga cagcacatat ctctcctcct ctctatagaa gccgtatggg gccaatcgac 4420
 tctcatgggt agaccgtgcc cttttgacac ggggagaaaag agaacgaaaag gacacttgac 4480
 cgattcgtta ataaagccgt cccacctttt tctttaatgg caattcaaga agagaaaaac 4540
 aacccctgcg cgcactcgag tagtcgatca gaccttccga acgacagata tcatttgctg 4600
 aaatcgaccg gattttaaag ctgctgccag gtcggtgaat ccccctaggt gatctccttg 4660

sequencelisting-21407.ST25

tacaaagatg ttgggcacgg acttttcgac ccggatgaga acgtcgtgaa gagtttgaaa 4720
 aagattatca acataatgtg tctttttttc ttttttcttt cgtaactctc tagagaacga 4780
 ggagacgtac ggtctgattt gttatcg 4807

<210> 2

<211> 1536

<212> DNA

<213> Phaffia rhodozyma

<220>

<221> CDS

<222> (1)..(1536)

<223>

<400> 2

atg ggc ata tca gat tac ctc gtt ctg gct ttc acg cat cct gcc gat 48
 Met Gly Ile Ser Asp Tyr Leu Val Leu Ala Phe Thr His Pro Ala Asp
 1 5 10 15

ctg cga gct tta atg cag tac gcg atc tgg cat gag cct cga agg aat 96
 Leu Arg Ala Leu Met Gln Tyr Ala Ile Trp His Glu Pro Arg Arg Asn
 20 25 30

atc act gca cag gag gaa cat gca aca tcc ggt tgg gac cga gaa act 144
 Ile Thr Ala Gln Glu Glu His Ala Thr Ser Gly Trp Asp Arg Glu Thr
 35 40 45

atg aag gaa tgt tgg aag tat ttg gat ctg act tca aga agt ttc gca 192
 Met Lys Glu Cys Trp Lys Tyr Leu Asp Leu Thr Ser Arg Ser Phe Ala
 50 55 60

gct gtc atc aaa gag ttg gac gga gat ctt acc cga gtc atc tgt tta 240
 Ala Val Ile Lys Glu Leu Asp Gly Asp Leu Thr Arg Val Ile Cys Leu
 65 70 75 80

ttc tat ctc gct ctt cga gga ctg gat acc att gag gat gac atg agt 288
 Phe Tyr Leu Ala Leu Arg Gly Leu Asp Thr Ile Glu Asp Asp Met Ser
 85 90 95

cta tct aat gat gtg aag ctt ccc ctg ctt cgg aca ttc tgg gaa aag 336
 Leu Ser Asn Asp Val Lys Leu Pro Leu Leu Arg Thr Phe Trp Glu Lys
 100 105 110

ctt gac tcc cct ggg tgg acc ttt act gga tcc ggt cca aat gag aag 384
 Leu Asp Ser Pro Gly Trp Thr Phe Thr Gly Ser Gly Pro Asn Glu Lys
 115 120 125

gat aga gag ctt ctt gtt cac ttc gat gtg gcc atc gcc gag ttt gcc 432
 Asp Arg Glu Leu Leu Val His Phe Asp Val Ala Ile Ala Glu Phe Ala
 130 135 140

aac ttg gac gtc aac tct cgg aac gtc att cga gac atc act cgc aag 480
 Asn Leu Asp Val Asn Ser Arg Asn Val Ile Arg Asp Ile Thr Arg Lys
 145 150 155 160

sequencelisting-21407.ST25

atg ggt aac ggt atg gcc gac ttt gct tct ctc tct acg ccc tcc aag	528
Met Gly Asn Gly Met Ala Asp Phe Ala Ser Leu Ser Thr Pro Ser Lys	
165 170 175	
cct gtg gcc gag gtc cag tcg acc gaa gat ttc aac cta tac tgt cat	576
Pro Val Ala Glu Val Gln Ser Thr Glu Asp Phe Asn Leu Tyr Cys His	
180 185 190	
tac gtc gct gga ctc gtc ggc gag gga ctc tcc cga ctc ttt gtc gcg	624
Tyr Val Ala Gly Leu Val Gly Glu Gly Leu Ser Arg Leu Phe Val Ala	
195 200 205	
acc gag aag gaa cga cca ttc ttg gcc aac cag atg gta ctt tca aac	672
Thr Glu Lys Glu Arg Pro Phe Leu Ala Asn Gln Met Val Leu Ser Asn	
210 215 220	
tcg ttc gga ctc ctt ctc caa aag aca aac atc ctt cga gat att cgg	720
Ser Phe Gly Leu Leu Leu Gln Lys Thr Asn Ile Leu Arg Asp Ile Arg	
225 230 235 240	
gag gac gcc gac gaa ggt cgt ggc ttc tgg cca aga gag atc tgg gcc	768
Glu Asp Ala Asp Glu Gly Arg Gly Phe Trp Pro Arg Glu Ile Trp Ala	
245 250 255	
aac ccg atc tat act gcg cat gca ccg ggc aca agg ttt aac tcg ttg	816
Asn Pro Ile Tyr Thr Ala His Ala Pro Gly Thr Arg Phe Asn Ser Leu	
260 265 270	
act gac ctg gtc aag aaa gaa aac atc gac aaa gga tca atg tgg gtg	864
Thr Asp Leu Val Lys Lys Glu Asn Ile Asp Lys Gly Ser Met Trp Val	
275 280 285	
ttg agt gcg atg aca ctc gac gcg atc acc cat act acc gac gca ctg	912
Leu Ser Ala Met Thr Leu Asp Ala Ile Thr His Thr Thr Asp Ala Leu	
290 295 300	
gac tac ctc tca ctt cta aag aac cag agt gtt ttc aac ttt tgt gct	960
Asp Tyr Leu Ser Leu Leu Lys Asn Gln Ser Val Phe Asn Phe Cys Ala	
305 310 315 320	
atc ccg gct gtc atg tcg att gca acg ttg gag cta tgc ttc atg aac	1008
Ile Pro Ala Val Met Ser Ile Ala Thr Leu Glu Leu Cys Phe Met Asn	
325 330 335	
cca gcg gtg ttc caa cga aac ata aaa atc aga aag gga gaa gcc gtc	1056
Pro Ala Val Phe Gln Arg Asn Ile Lys Ile Arg Lys Gly Glu Ala Val	
340 345 350	
gag ctc att atg aag tgc aac aac cct cgg gag gtg gca tac atg ttt	1104
Glu Leu Ile Met Lys Cys Asn Asn Pro Arg Glu Val Ala Tyr Met Phe	
355 360 365	
aga gat tat gct cga aag att cat gcc aag gct att cct aca gat cct	1152
Arg Asp Tyr Ala Arg Lys Ile His Ala Lys Ala Ile Pro Thr Asp Pro	
370 375 380	
aac ttc atc aag ttg agc gtt gcg tgt ggt cga atc gaa caa tgg gct	1200
Asn Phe Ile Lys Leu Ser Val Ala Cys Gly Arg Ile Glu Gln Trp Ala	
385 390 395 400	
gag cac tac tac ccc tca ttt atg atg att cgg cct tcg aat gac cct	1248
Glu His Tyr Tyr Pro Ser Phe Met Met Ile Arg Pro Ser Asn Asp Pro	
405 410 415	
caa aac ccc gca ccc tca acg gcg ctt gac cct ttc tca gga gac gct	1296
Gln Asn Pro Ala Pro Ser Thr Ala Leu Asp Pro Phe Ser Gly Asp Ala	
420 425 430	

sequencelisting-21407.ST25

```

cgt tta agg ata gcc tct aag aag gct gag atc acc gcc gct gct ctt      1344
Arg Leu Arg Ile Ala Ser Lys Lys Ala Glu Ile Thr Ala Ala Ala Leu
      435      440      445

gtc agg aag aaa gcc cgg gat cac gct aag tgg aga gag tcc aag gga      1392
Val Arg Lys Lys Ala Arg Asp His Ala Lys Trp Arg Glu Ser Lys Gly
      450      455      460

ttg cct ccg agc gat ccg aac aag ccg gac aac tcg gag gat gtt aat      1440
Leu Pro Pro Ser Asp Pro Asn Lys Pro Asp Asn Ser Glu Asp Val Asn
      465      470      475

tgg gta ttg atc ggc ggt atg atc gtt gga ttg ttg ctc gtg atg ggc      1488
Trp Val Leu Ile Gly Gly Met Ile Val Gly Leu Leu Leu Val Met Gly
      485      490      495

gtg ctc ggt ttg gct atc gct tgg gtt gtt ctt cag ttt gag caa taa      1536
Val Leu Gly Leu Ala Ile Ala Trp Val Val Leu Gln Phe Glu Gln
      500      505      510

```

<210> 3

<211> 511

<212> PRT

<213> Phaffia rhodozyma

<400> 3

```

Met Gly Ile Ser Asp Tyr Leu Val Leu Ala Phe Thr His Pro Ala Asp
1      5      10      15

Leu Arg Ala Leu Met Gln Tyr Ala Ile Trp His Glu Pro Arg Arg Asn
      20      25      30

Ile Thr Ala Gln Glu Glu His Ala Thr Ser Gly Trp Asp Arg Glu Thr
      35      40      45

Met Lys Glu Cys Trp Lys Tyr Leu Asp Leu Thr Ser Arg Ser Phe Ala
50      55      60

Ala Val Ile Lys Glu Leu Asp Gly Asp Leu Thr Arg Val Ile Cys Leu
65      70      75      80

Phe Tyr Leu Ala Leu Arg Gly Leu Asp Thr Ile Glu Asp Asp Met Ser
      85      90      95

Leu Ser Asn Asp Val Lys Leu Pro Leu Leu Arg Thr Phe Trp Glu Lys
      100      105      110

Leu Asp Ser Pro Gly Trp Thr Phe Thr Gly Ser Gly Pro Asn Glu Lys
      115      120      125

Asp Arg Glu Leu Leu Val His Phe Asp Val Ala Ile Ala Glu Phe Ala
130      135      140

```

sequence listing-21407.ST25

Asn Leu Asp Val Asn Ser Arg Asn Val Ile Arg Asp Ile Thr Arg Lys
 145 150 155 160
 Met Gly Asn Gly Met Ala Asp Phe Ala Ser Leu Ser Thr Pro Ser Lys
 165 170 175
 Pro Val Ala Glu Val Gln Ser Thr Glu Asp Phe Asn Leu Tyr Cys His
 180 185 190
 Tyr Val Ala Gly Leu Val Gly Glu Gly Leu Ser Arg Leu Phe Val Ala
 195 200 205
 Thr Glu Lys Glu Arg Pro Phe Leu Ala Asn Gln Met Val Leu Ser Asn
 210 215 220
 Ser Phe Gly Leu Leu Leu Gln Lys Thr Asn Ile Leu Arg Asp Ile Arg
 225 230 235 240
 Glu Asp Ala Asp Glu Gly Arg Gly Phe Trp Pro Arg Glu Ile Trp Ala
 245 250 255
 Asn Pro Ile Tyr Thr Ala His Ala Pro Gly Thr Arg Phe Asn Ser Leu
 260 265 270
 Thr Asp Leu Val Lys Lys Glu Asn Ile Asp Lys Gly Ser Met Trp Val
 275 280 285
 Leu Ser Ala Met Thr Leu Asp Ala Ile Thr His Thr Thr Asp Ala Leu
 290 295 300
 Asp Tyr Leu Ser Leu Leu Lys Asn Gln Ser Val Phe Asn Phe Cys Ala
 305 310 315 320
 Ile Pro Ala Val Met Ser Ile Ala Thr Leu Glu Leu Cys Phe Met Asn
 325 330 335
 Pro Ala Val Phe Gln Arg Asn Ile Lys Ile Arg Lys Gly Glu Ala Val
 340 345 350
 Glu Leu Ile Met Lys Cys Asn Asn Pro Arg Glu Val Ala Tyr Met Phe
 355 360 365
 Arg Asp Tyr Ala Arg Lys Ile His Ala Lys Ala Ile Pro Thr Asp Pro
 370 375 380
 Asn Phe Ile Lys Leu Ser Val Ala Cys Gly Arg Ile Glu Gln Trp Ala
 385 390 395 400
 Glu His Tyr Tyr Pro Ser Phe Met Met Ile Arg Pro Ser Asn Asp Pro
 405 410 415

sequencelisting-21407.ST25

Gln Asn Pro Ala Pro Ser Thr Ala Leu Asp Pro Phe Ser Gly Asp Ala
 420 425 430

Arg Leu Arg Ile Ala Ser Lys Lys Ala Glu Ile Thr Ala Ala Ala Leu
 435 440 445

Val Arg Lys Lys Ala Arg Asp His Ala Lys Trp Arg Glu Ser Lys Gly
 450 455 460

Leu Pro Pro Ser Asp Pro Asn Lys Pro Asp Asn Ser Glu Asp Val Asn
 465 470 475 480

Trp Val Leu Ile Gly Gly Met Ile Val Gly Leu Leu Leu Val Met Gly
 485 490 495

Val Leu Gly Leu Ala Ile Ala Trp Val Val Leu Gln Phe Glu Gln
 500 505 510

<210> 4

<211> 27

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<222> (3)..(3)

<223> n = a, c, g or t

<220>

<221> misc_feature

<222> (4)..(4)

<223> y = c or t

<220>

<221> misc_feature

<222> (6)..(6)

<223> n = a, c, g or t

<220>

sequencelisting-21407.ST25

<221> misc_feature

<222> (12)..(12)

<223> n = a, c, g or t

<220>

<221> misc_feature

<222> (15)..(15)

<223> n = a, c, g or t

<400> 4

gcnytngaya cngtngarga ygayatg

27

<210> 5

<211> 26

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<222> (3)..(3)

<223> n = a, c, g or t

<220>

<221> misc_feature

<222> (9)..(9)

<223> n = a, c, g or t

<220>

<221> misc_feature

<222> (15)..(15)

<223> n = a, c, g or t

<220>

<221> misc_feature

<222> (18)..(18)

sequencelisting-21407.ST25

<223> n = a, c, g or t

<220>

<221> misc_feature

<222> (21)..(21)

<223> n = a, c, g or t

<400> 5

atngccatna cytgnggnat ngcrca

26

<210> 6

<211> 29

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<222> (3)..(3)

<223> n = a, c, g or t

<220>

<221> misc_feature

<222> (6)..(6)

<223> n = a, c, g or t

<220>

<221> misc_feature

<222> (9)..(9)

<223> n = a, c, g or t

<220>

<221> misc_feature

<222> (12)..(12)

<223> n = a, c, g or t

sequencelisting-21407.ST25

<220>

<221> misc_feature

<222> (15)..(15)

<223> n = a, c, g or t

<400> 6

ccnacngtnc cngcnacrta rtgrcarta

29

<210> 7

<211> 20

<212> DNA

<213> Artificial

<400> 7

aatgatgtga agcttcccct

20

<210> 8

<211> 20

<212> DNA

<213> Artificial

<400> 8

ccagatctct cttggccaga

20